

DC921 U.S. PRO  
09/834792



04/13/01

Figure 1  
(Sheet 1 of 17)

AP32911

MOTTQSSCPGSPFDTEDCWEI JLCRGEINFGGSGKKRKGKFKVVFSSVAFSVLFELLLTEWELFAPNLVVSLVGEERPLAMKSWLRDVL  
KGLVKAAGSTGAWILTSALHVGLARHVGCAYKDHSLASTSTKI KVVAI GMS LDFJ LHKQLLDGVHOKEDTFI HYPADENI QGPLCPI  
DENLEHFI LVEFGALGSGNDGLTELQLSLEKHI SQORTGYGGTSCIOI FVLC LLVNGDPNTLEKIS RAVEQAPWLI LAGSGGI ADVLA  
ALVSO PHLLVPQVAEKQFREKFFSECF SWEAJ VHWTELLQNI AAHFHLLTVYDFEQEGSEDLDTVI LKALVKACKSHSQEAQDYLDLY  
LAVAWDRVDEJ AKSEI JNGDVIEWKSCDLEEVMT DALVSNKFDVRLFVDSGADMAEFLTYGFLQCLYHSVSFKSLLFELLQKHEEGRLT  
LAGLGAQQARELPJ CLFAFSLHVSRLVKDFLHDACHGFI YODGRKMEERGFPRFI AGOKWLFELSKKSEDPWRDLFLWAVLQNRMYEMATY  
FWLMGFEGVAAALACKJIKEMSHLEKLAIVAKTMRKAKYEQLALDLTSECYGNSEDFAFALLVKNHNSWSRTTCLHLATEADAKAFFA  
HDGVQAFITKJWWGDMATGTPJLALLEGAFTHALIYTNLI STSEDAPQMDLEDLQEPDSIDMEKSLC SRGGQLEKLTEAPRAPGDLG  
FOAFLLTFWKKTFWGAFTVFLGNVVMYI AFLFLFTYVLLVDFFFPQGFSGSEVTLYFWVFTLVLEEJ RQGFFTDEDTHLVKKFTLYV  
EDRWKNC DMVAJ FLFI VGVTCRMVPSVFLAGRTVLAJDFMVFTLRLLI HIFAJHKQLGPKI I VERMMKDVFFLFFLSVWLVAYGVTTQ  
ALLHFDGKLEWJ FRVLYKPYLQIFGQIFLDEJDLARVNC SLHPLLLESSASC PNLYANWLVI LLLVTFLVTNVLLMNLIIAMFSYT  
FQVVQGNADMTWKFORYHLIVLYHGRPALAPFFI LLSHLSELVLKQVFRKLAQHKKQHLEKDLDFDLDOKI ITWETVOKENFLSTMEKRA  
RDESEGEVLKRTAHKVDLIAKYI GGLREGEKHI KCLESCANYCMILLSSMTDT LAPGGTYSSSQNGCRSQPASARDREYLESGLPPSDT

Figure 2  
(Sheet 2 of 17)  
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## Human TRF1 nucleotide sequence

SEQ New: 3498 bp;

Composition: 634 A; 1089 C; 1143 G; 632 T; 0 OTHER

Percentage: 18% A; 31% C; 33% G; 18% T; 0% OTHER

Molecular Weight (kDa): ssDNA: 1081.34 dsDNA: 2157.1

ORIGIN

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1   ATGCAGGATG TCCAAGGCC CCGTCCCGGA AGCCCCGGGG ATGCTGAAGA CCGGCGGGAG
2   CTGGGCTTGC ACAGGGGCGA GGTCAACTTT GGAGGCTCTG GGAAGAAGCG AGGCAAGTTT
3   GTACGGGTGC CGAGCGGAGT GCGCCGCTCT GTGCTCTTTG ACCTGCTGCT TGCTGAGTGG
4   CACCTGCCGG CCCCCAACCT GGTGCTGTCC CTGGTGGGTG AGGAGCAGCC TTTCGCCATG
5   AAGTCTTGCC TCGCGGATGT GTCGCGCAAG GGGCTGCTGA AGGCGGCTCA GAGCACAGGA
6   GCCTGGATCC TGACCAATGC CCTCCGCGTG GGCCTGGCCA GGCAATCGG GCAGGCCGTG
7   CGCGACCACT CGCTGGCCAG CACGTCCACC AAGGTCCCTG TGTTGCTGT CGGCATGGCC
8   TCGCTGGGCC GCGTCTGCA CCGCCGATT CTGGAGGAGG CCCAGGAGGA TTTTCCTGTG
9   CACTACCCTG AGGATGACGG CGGCAGCCAG GGCCCCCTCT GTTCACTGGA CAGCAACCTG
10  TCCCACTTCA TCCTGCTGGA GCCAGGCCCC CCGGGGAGG GCGATGGGCT GACGGAGCTG
11  CGGTGAGGC TGGAGAAGCA CATCTCGAG CAGAGGGCGG GCTACGGGGG CACTGGCAGC
12  ATCGAGATCC CTGTCTCTG CTCTCTGCTC AATGGTGATC CCAACACCTT GGAGAGGATC
13  TCCAGGGCCG TGGAGCAGGC TGCCCCGTGG CTGATCCTGG TAGGCTCGGG GGGCATCGCC
14  GATGTCTTTC CTGCCCTAGT GAACCAAGCC CACCTCCTGG TGCCCAAGGT GGCCGAGAAC
15  CAGTTTAAGG AGAAGTTCCC CAGCAAGCAT TTCTCTTGGG AGGACATCGT GCGCTGGACC
16  AAGTCTCTGC AGAACATCAC CTCACACCAG CACCTGCTCA CCGTGTATGA CTTCCGAGCA
17  GAGGGCTCCG AGGAGCTGGA CACGGTCATC CTGAAGGCGC TGGTGAAAGC CTGCAAGAGC
18  CACAGCCAGG AGCCTCAGGA CTATCTGGAT GAGCTCAAGC TGGCCGTGGC CTGGGACCGC
19  GTGGACATCG CCAAGAGTGA GATCTTCAAT GGGGACCTGG AGTGGAAATC CTGTGACCTG
20  GAGGAGGTGA TGCTGGACGC CCTGGTCAAG AACAAAGCCC AGTTTGTGCG CCTCTTTGTG
21  GACAACGGCG CAGACGTGGC GACTTCTCTG ACCTATGGGC GGCTGCAGGA GCTCTACCGC
22  TCCGTGTACG GCAAGAGCCT GCTCTTCGAG CTGCTGCAGC GGAAGCAGGA GGAGGCCCGC
23  CTGACGCTGG CCGGCCTGGG CACCCAGCAG GCCCGGGAGC CACCCGCGGG GCCACCGGCC
24  TTCTCCCTGC ACGAGGTCTC CCGGCTACTC AAGGACTTCC TGCAGGACGC CTGCCGAGGC
25  TTCTACCAGG ACGGCCGGCC AGGGGACC GC AGGAGGGCGG AGAAGGGCCC GGCCAAGCGC
26  CCCACGGGCC AGAAGTGGCT GCTGGACCTG AACCAGAAGA GCGAGAACCC CTGGCGGGAC
27  CTGTTCTCTG GGGCCGTGCT GCAGAACC GC CACGAGATGG CCACCTACTT CTGGGCCATG
28  GGCCAGGAAG GTGTGGCAGC CGACTGGCC GCCTGCAAAA TCCTCAAAGA GATGTGCAC
29  CTGGAGACGG AGGCCGAGGC GGCCCGAGCC ACGCGCGAGG CGAAATACGA GCGGCTGGCC
30  CTTGACCTCT TCTCCGAGTG CTACAGCAAC AGTGAGGCC GCGCCTTCGC CCTGCTAGTG
31  CGCCGGAACC GCTGCTGGAG CAAGACCACC TGCTGCACC TGGCCACCGA GGTCAGGCC
32  AAGGCCTTCT TTGCCCACGA CGCGGTTGAG GCCTTCCTGA CCAGGATCTG TTGGGGGGAC
33  ATGGCCGCGA GCACGCCAT CTGCGGCTG CTAGGAGCCT TCCTCTGCCC CGCCCTCGTC
34  TATACCAACC TCATCACCTT CAGTGAGGAA GCTCCCCTGA GGACAGGCCT GGAGGACCTG
35  CAGGACCTGG ACAGCCTGGA CACCGAGAAG AGCCCGCTGT ATGGCCTGCA GAGCCGGGTG
36  GAGGAGCTGG TGGAGGCGCC GAGGGCTCAG GGTGACCGAG GCCACGTGC TGTCTTCTG
37  CTCACACGCT GGCGGAAATT CTGGGGCGCT CCCGTGACTG TGTTCTTGGG GAACGTGGTC
38  ATGTACTTCG CCTTCCTCTT CTTGTTTACC TACGTCTTGC TGGTGGACTT CAGGCCGCCC
39  CCCAGGGGCC CCTCAGGGCC CGAGGTCACC CTCTACTTCT GGGTCTTTAC GCTGGTGCTG
40  GAGGAAATCC GGCAGGGCTT CTTACAGAC GAGGACACAC ACCTGGTGAA GAAGTTCACA
41  CTGTATGTGG GGGACAAC TG GAACAAGTGT GACATGGTGG CCATCTTCTT GTTCATCGTG
42  GGTCTCACCT GCAGGATGCT GCCGTGGCGG TTTGAGGCTG GCCGCACGGT CCTCGCCATG
43  GAGTTTATGG TGTTACAGCT GCGGCTGATC CATATCTTTG CCATACACAA GCAGCTGGGC
44  CCCAAGATCA TCGTGGTAGA GCGCATGATG AAGGACGTCT TCTTCTTCTT CTTCTTTCTG
45  AGCGTGTGCG TCGTGGCCTA CGGTGTACAC ACCGAGGCGC TGCTGCACCC CCATGACGGC
46  CGCCTGGAGT GGATCTTCCG CCGGGTGCTC TACCGGCCCT ACCTGCAGAT CTTGCGCCAG
47  ATCCCACTGG ACAGATTGA TGAAGCCCGT GTGAAGTGT CCACCCACCC ACTGCTGCTG
48  GAGGACTCAC CATCTGCC CAGCCTCTAT GCCAAGTGGC TGGTCATCCT CTTGCTGGTC
49  ACCTTCTGTG TGGTGAAGAA TGTGCTGCTG ATGAACCTGC TCATCGCCAT GTTCAGCTAC
50  ACGTTCACAG TGGTGCAGGG CAACGCAGAC ATGTTCTGGA AGTTCACGCG CTACAACCTG

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Figure 3A  
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300. ATTCTCGAGT ACCACGAGCG CCCCGCCCTG CCCCCGCCCT TCATCCTGCT CAGCCACCTG  
 300. AGCCTGACGC TCCGCCGGGT CTTCAAGAGG GAGGCTGAGC ACAAGCGGGA GCACCTGGAG  
 310. AGAGACCTGC CAGACCCCTT GGACCAGAGG GTCTCTACCT GGGAGACAGT CCAGGAGGAG  
 310. AACTTCCTGA CCAAGATGGA GAAGCGGAGG AGCGACAGCG AGGGGGAGGT GCTGCGGAA  
 320. ACCGCCACA GAGTGGACTT CATTGCCAAG TACCTCGGGG GGCTGAGAGA GCAAGAAAAG  
 330. CGCATCAAGT GTCTGAGTC ACAGATCAAC TACTGCTCGG TGCTCGTGTC CTCCGTGGCT  
 330. GACGTGCTGG CCCAGGCTGG CGGCCCCCGG AGCTCTCAGC ACTGTCCGGA GGAAGCCAG  
 340. CTGGTGGCTG CTGACCACAG AGGTGGTTTA CATGGCTGGG AACAAACCCG GGCTGGCCAG  
 340. CCTCCCTCGG ACACATCA

Figure 3B  
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Human TEF8 protein coding sequence  
 Translation of Htrp8coding(1-3498)  
 Universal code  
 Total amino acid number: 1165, MW=13128:  
 Max ORF: 1-3495, 1165 AA, MW=13128:

ORIGIN

1	MQDVQGFRPG	SPGDAEDERE	LGLHFGENVF	GGSGKKRGKF	VRVPSGVAPS
10	VLFDLILAEW	HLFAFNLVVS	LVGEELOFFAM	KSWLRDVLAK	GLVKAAQSTG
100	AWILTSALRV	GLARHVGQAV	RDHSLASTST	KVRVVAVGMA	SLGRVLHRRK
110	LEEAQEDFPV	HYPEDDCGSQ	GFLCSLDSNL	SHFILVEPGP	PGKGDGLTEL
200	RLALEKHISE	QRAGYGGTGS	IEIFVLCLLV	NGDPNTLEKJ	SKAVEQAAPW
250	LILVSGGGA	DVLAALVNQF	HLLVPKVAEK	QFKEKFPSKH	FSWEDIVRWI
300	KLLQNTSHQ	HLLTVYDFEQ	EGSEELDTVI	LKALVKACKS	HSQEPQDYLI
350	ELKLAVAWDF	VDIAKSEIFN	GDVEWKSCDL	EEVMVDALVS	NKPEFVRLFV
400	DNGADVADFL	TYGRLQELYK	SVSRKSELLFD	LLQKQOEER	LTLAGLGTOQ
450	AREFFAGFFA	FSLHEVSRVL	KDFLODACRG	FYQDGRPGDR	RRAEKGPAPK
500	PTGQKWLLDL	NQKSENFWRD	LFLWAVLQNF	HEMATYFWAM	GOEGVAAALA
550	ACKILKEMSH	LETEAEAAKA	TREAKYERLA	LDLFSECYSN	SEARAFALLV
600	RKNKWSKTT	CLHLATEADA	KAFFAHDGVQ	AFLTRIWWGD	MAAGTPILRL
650	LGAFLCFALV	YTNLITFSEE	AFLATGLEDL	QDLDSLDEK	SPLYGLQSRV
700	EELVEAPRAQ	GDRGPRAVFL	LTRWKKFWGA	PVTVFLGNVV	MYFAFLFLFT
750	YVLLVDFRPP	POGPSGFVET	LYFWVFTLV	EEIROGFFTD	EDTHLVKKFT
800	LYVGDNWNKC	DMVAIFLFIV	GVTCKMLPSA	FEAGRTVLAM	DFMVFTLRLI
850	EIFAHHKQLG	PKIIVVERMM	KDVFFFLFFL	SVWLVAYGVT	TQALLHPHDG
900	ELEWIFARVL	YRPYLQIFGQ	JPLDEIDEAR	VNCSTHPLLL	EDSPSCPSLY
950	ANWLVIILLV	TFLLVTVNLL	MNLLIAMFSY	TFQVVQGNAD	MFWKFORYNL
1000	IVEYHEAPAL	APPFILLSHL	SLTLARVFKK	EAHKKREHLE	RDLPLDPLDQY
1050	VVTWETVQKE	NFLSKMEKRR	RDSEGEVLAK	TAHRVDFIAK	YLGGLREOEK
1100	RIKCLESQIN	YCSVLVSSVA	DVLAQCGGPR	SSQHCGECSQ	LVAADHRGGI
1150	DGWEQPGAGQ	PPSDT*			

Figure 4  
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Figure 1 - Comparison of the amino acid sequences of mouse and human TRF1

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mTf1:  MCTTCSFCHGSIITLIDGWEIILCHGINTFCGSGHGHGFVNVFSSVAFSVLFELLITTEW 60
hTf1:  MGEVQGFAPGSPGDALDERELGLHGEVNIQGSCHKFGKFRVVPSPGVLPVLFDLLLAEW 60
      * * * * *

mTf1:  ELFAFNLVVSLNGELMPLAMKSWLRDVLKFGNVAACSTGAWIITSALHVGCLARHVGGAV 120
hTf1:  ELFAFNLVVSLNGELQTFAMKSWLRDVLKFGNVAACSTGAWIITSALFVGLARHVGGAV 120
      * * * * *

mTf1:  KDESIASTSTKIFVVAIGMASLDLILHACLLHGVHOKEDTFIHYFADEGNIQGFLCFLDS 180
hTf1:  KDESIACTSTKVEVVAIGMASLGRVLEHJILEAC--EDFPVHYPEDDGGSQGFLCFLDS 178
      * * * * *

mTf1:  NLSHFILVESGALGSGNDGLTELQSLERKHSQCKTGYGCTSCIQIPVLCLLVNGDPNTL 240
hTf1:  NLSHFILVEFGFPGK-DGLTELRLERKHSQCKAGYGGTGSIEIPVLCLLVNGDPNTL 237
      * * * * *

mTf1:  ERISRAVEQAAPWLIILACSGGIADVLAAALVSGFHLVFOVAEKQFKEKFPSECFSWEAIV 300
hTf1:  ERISRAVEQAAPWLIILVCSGGIADVLAAALVNGFHLVFKVAEKQFKEKFPSECFSWEDIV 297
      * * * * *

mTf1:  HWTELLQNIAAHFELLTVYDFEQEGSEDLTVILKALVKACKSHSQEAQDYLDLKLAVA 360
hTf1:  HWTELLQNI TSHQELLTVYDFEQEGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVA 357
      * * * * *

mTf1:  WDFVDIAKSEIFNGDEVWKSCLLEEVMTDAIVSNKEDFVRLFVDGADMAEFLTYGKLQO 420
hTf1:  WDFVDIAKSEIFNGDEVWKSCLLEEVMTDAIVSNKEDFVRLFVDNGADVADFLTYGKLQO 417
      * * * * *

mTf1:  LYKSVSFKSLLFELLQAKHEEGRLTLAGLGAQAELFI GLFAFSLHEVSRVLKDFLHDA 480
hTf1:  LYKSVSFKSLLFELLQAKHEEAKRLTLAGLGTQAELFFAGFFAFSLHEVSRVLKDFLQDA 477
      * * * * *

mTf1:  CKGFYQDGK----KMEIKGFKRFAGQKWLFEISKSEDFWRDLFLWAVLQNRKEMATYF 536
hTf1:  CKGFYQDGKPGDRKAAEKGFARPTGQKWLLELNQSENFWRDLLWAVLQNRKEMATYF 537
      * * * * *

mTf1:  WAMGREGVAAALAAACKI IKEMSHLEKEAEVARTMAEAKYEQLALDLFSECYGNSEDRAFA 596
hTf1:  WAMGQEGVAAALAAACKI LKEMSHLETEAAAKATREAKYERLALDLFSECYSNSEARAF 597
      * * * * *

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Figure 5  
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Classification and Secondary Structure Prediction of Membrane Protein:

<http://azusa.proteome.bio.tuat.ac.jp/sosui/>

Orientation of the N-terminus of mTrp8: IN  
 Number of transmembrane helices of mTrp8: 6  
 Position of transmembrane helices of mTrp8:

helix	begin	end
1	731	754
2	769	791
3	807	829
4	839	861
5	870	891
6	951	971

Orientation of the N-terminus of hTrp8: IN  
 Number of transmembrane helices of hTrp8: 6  
 Position of transmembrane helices of hTrp8:

helix	begin	end
1	731	751
2	770	791
3	807	829
4	841	861
5	871	891
6	951	971

Figure 6A  
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Hydrophobicity profile of mTrp8 (Made with DNAMAN software)

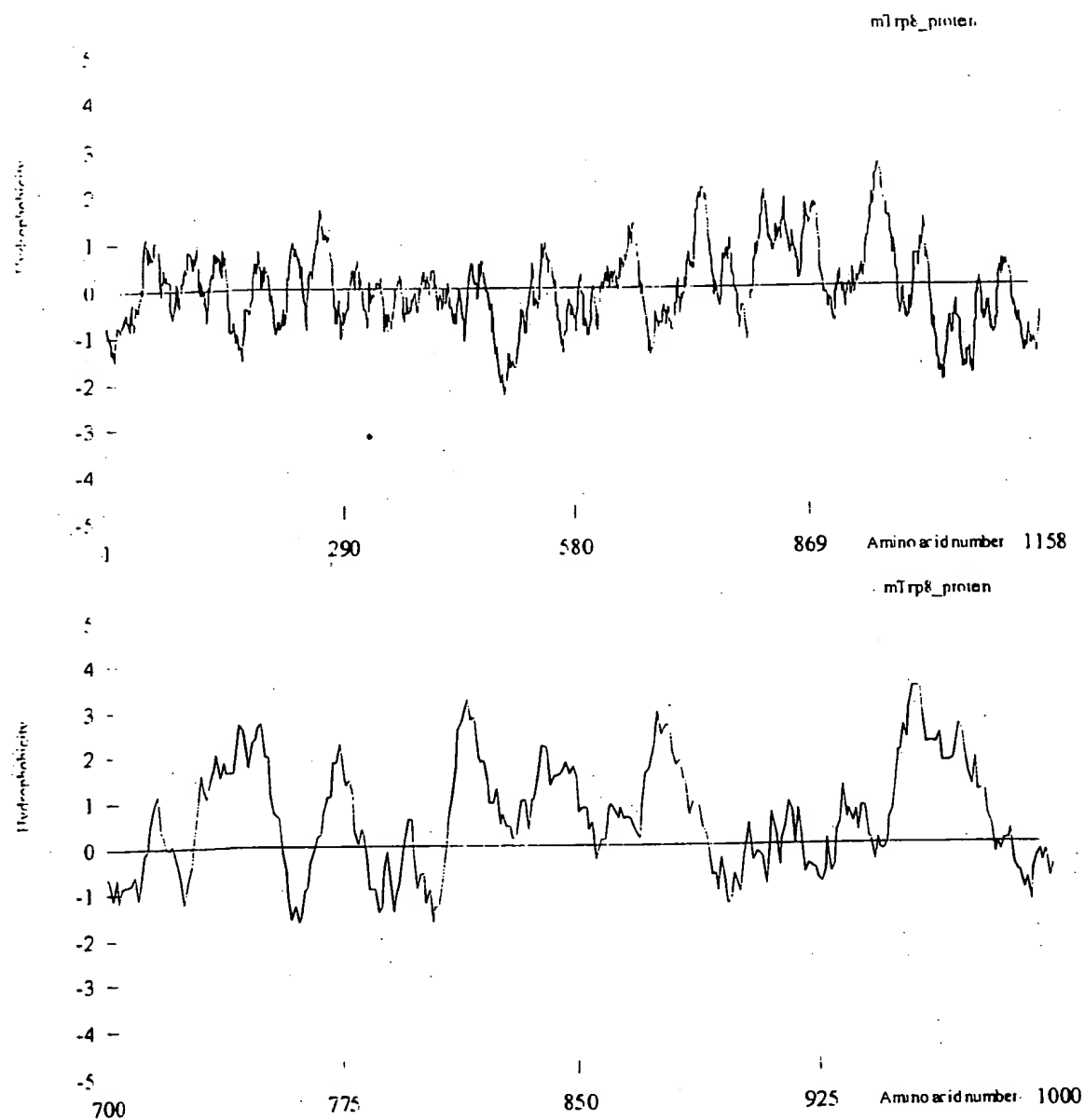


Figure 6B  
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Hydrophobicity profile of hTrpE (Made with DNAMAN software)

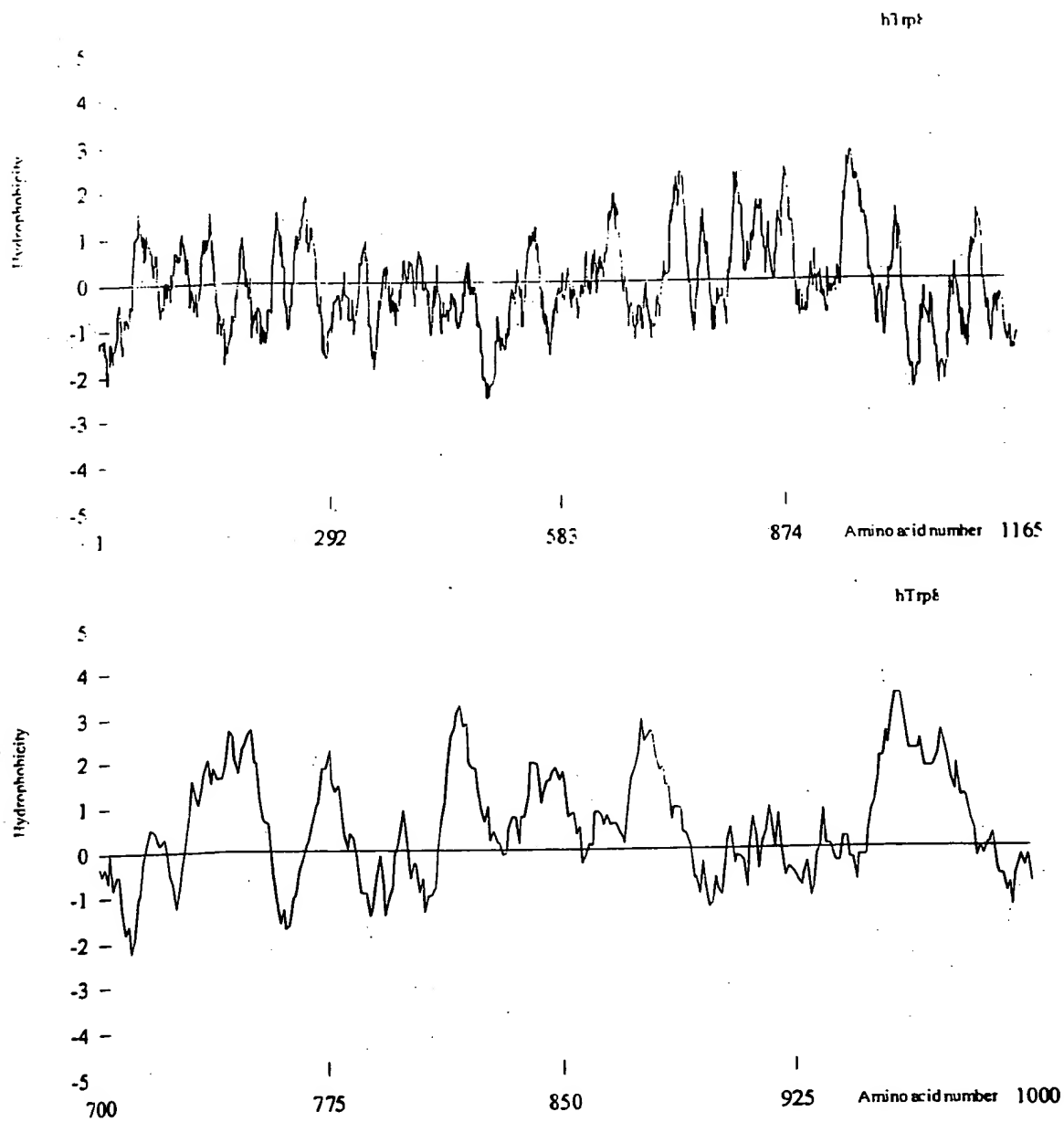


Figure 6C  
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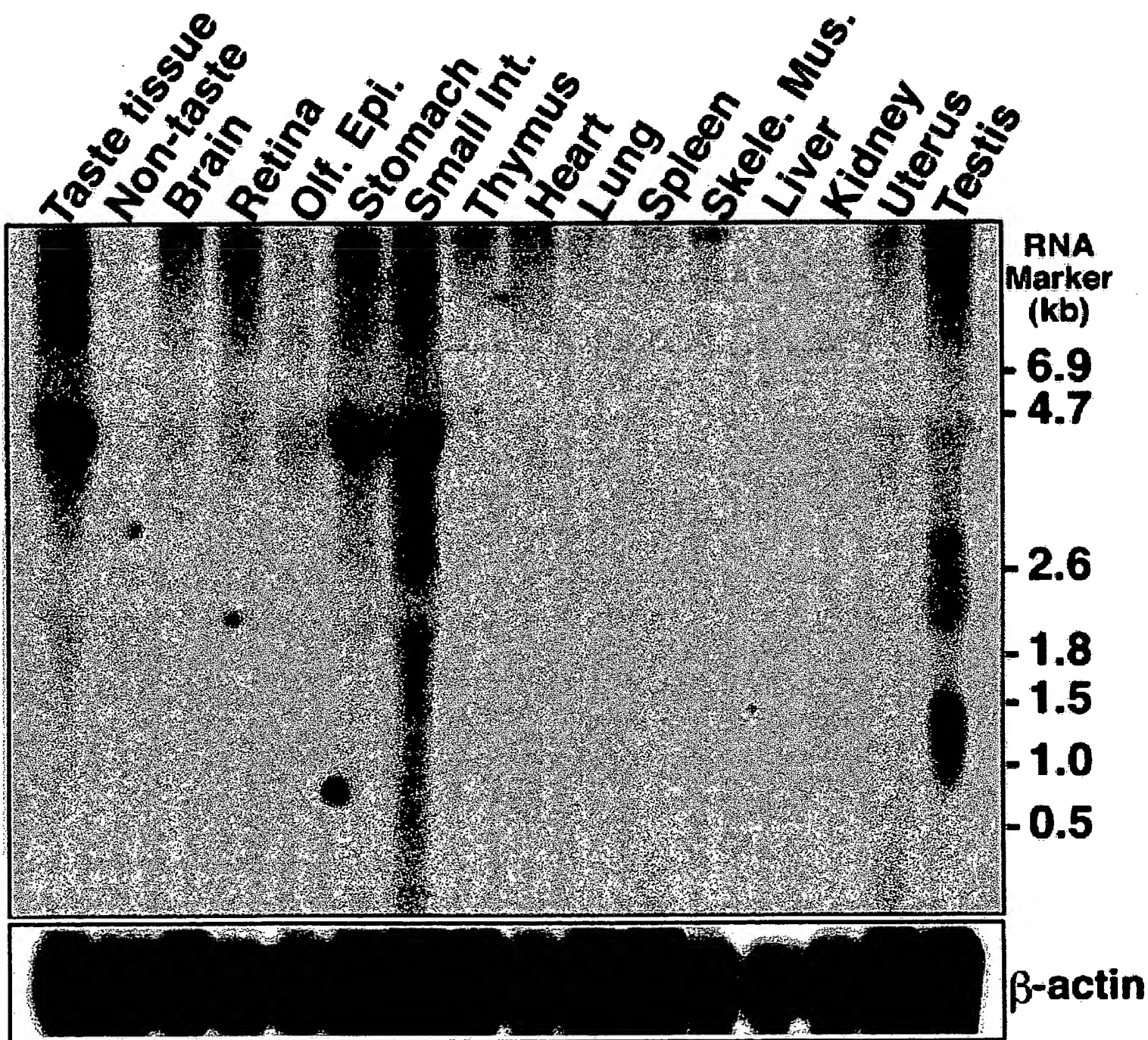


Figure 7  
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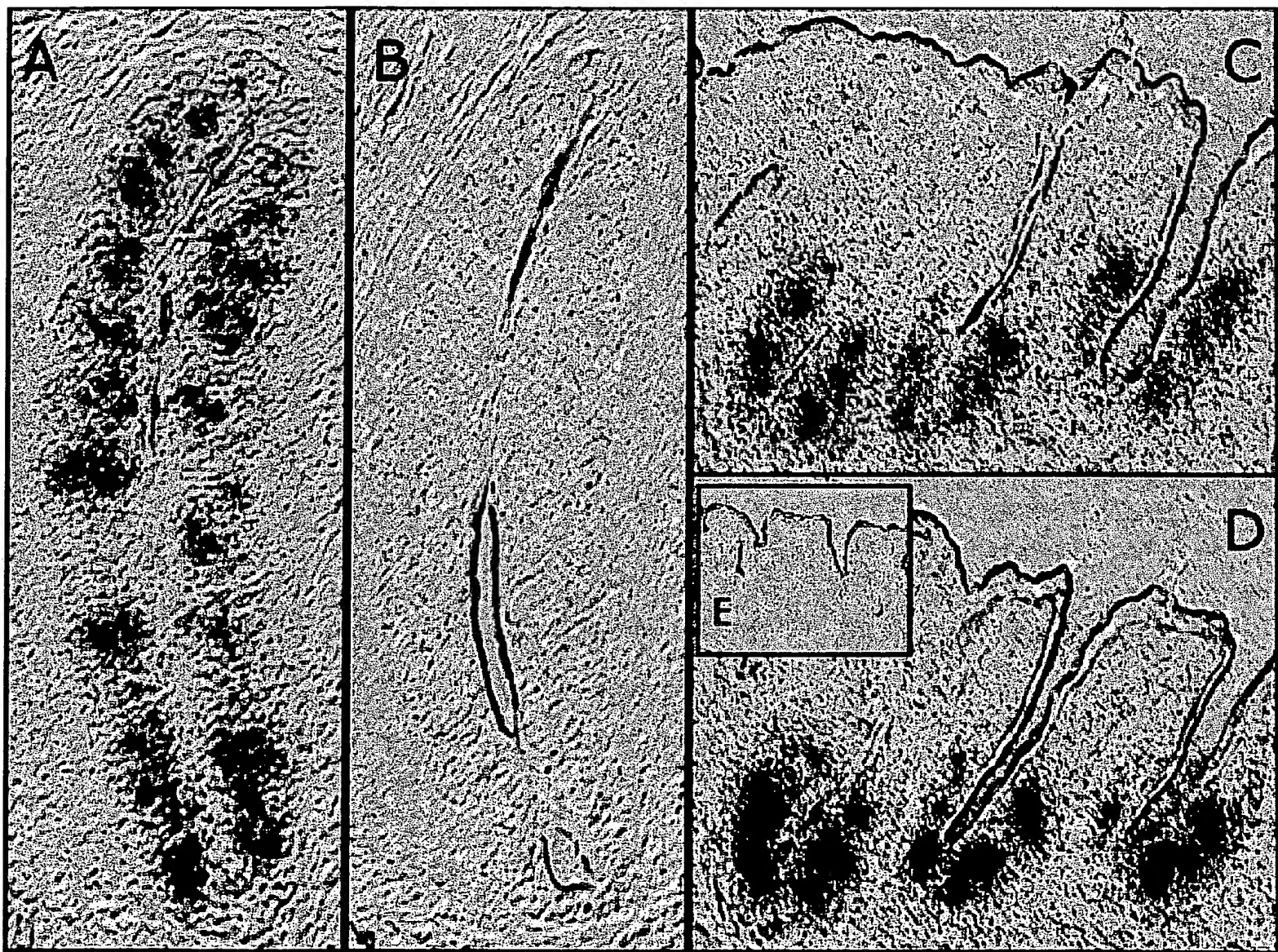


Figure 8  
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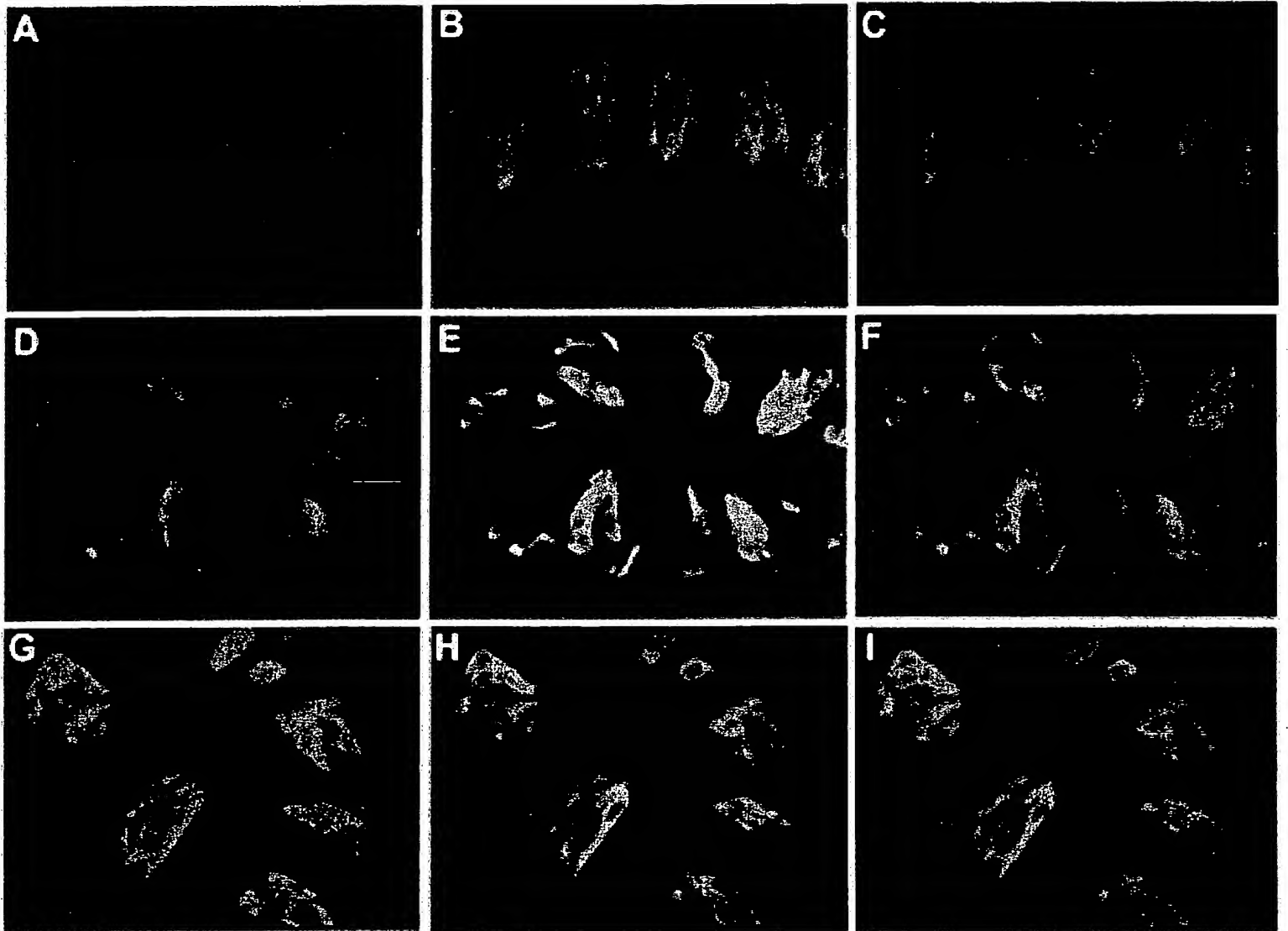


Figure 9  
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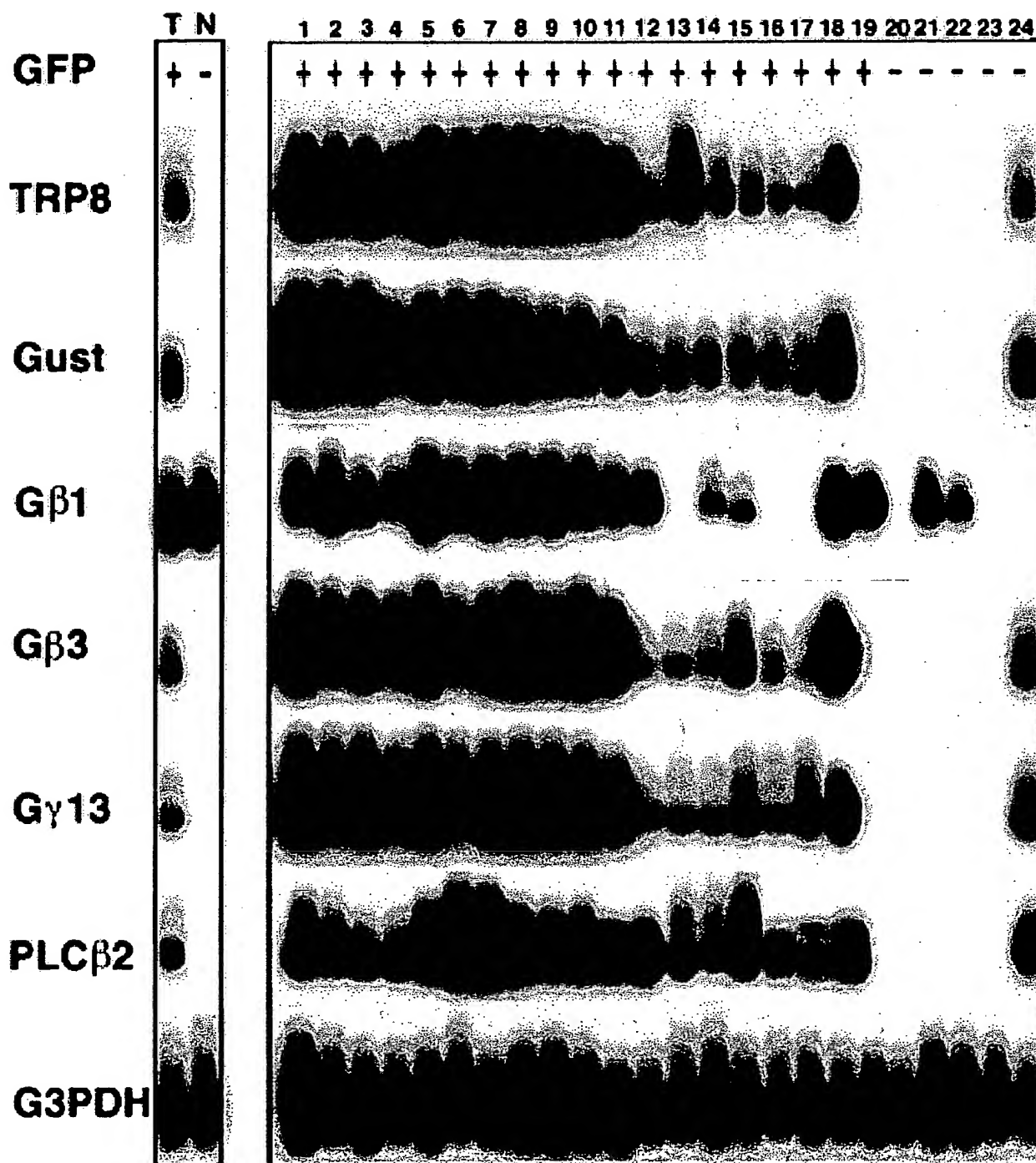


Figure 10  
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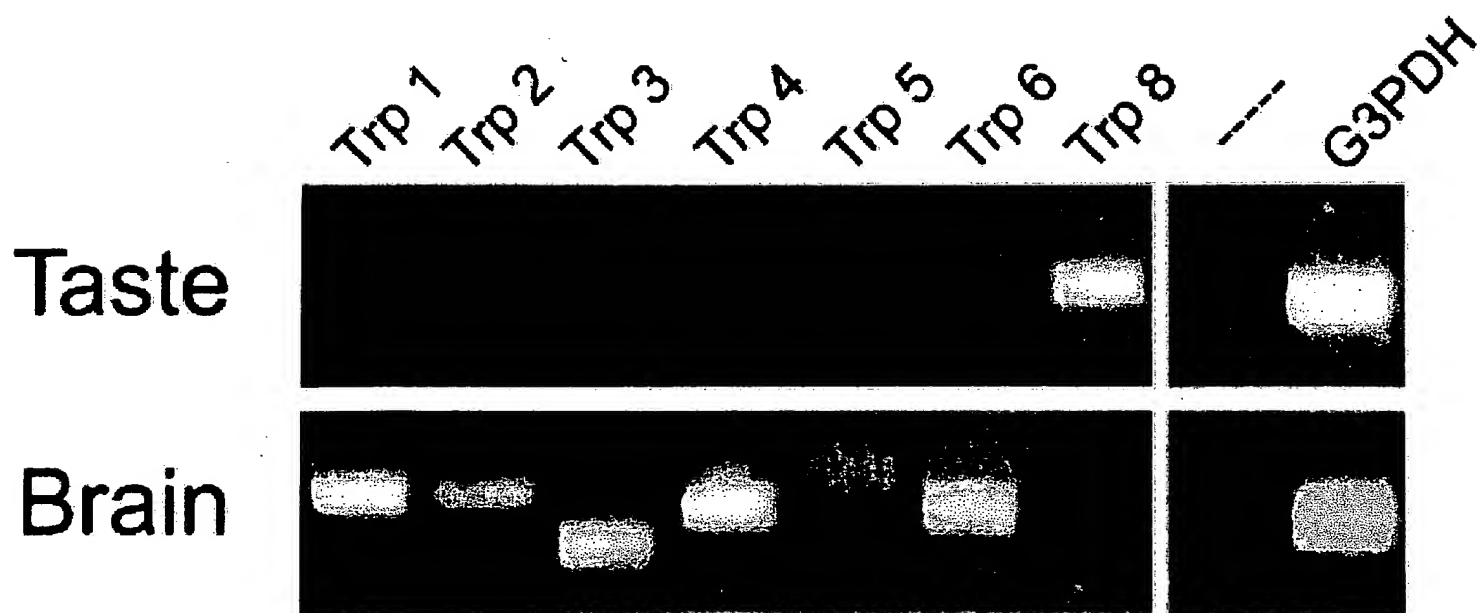


Figure 11  
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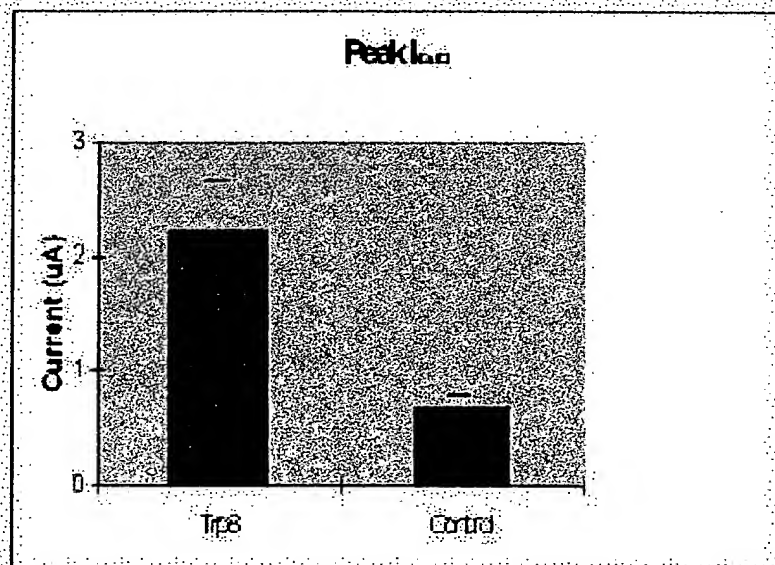
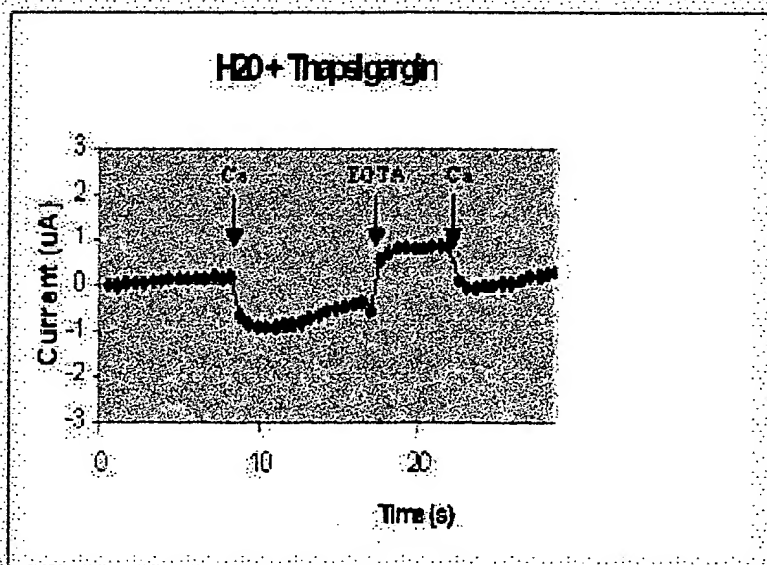
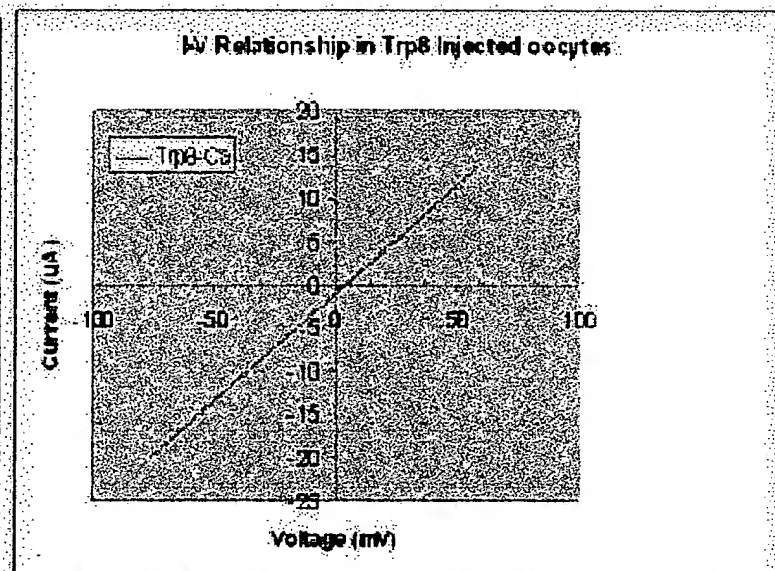
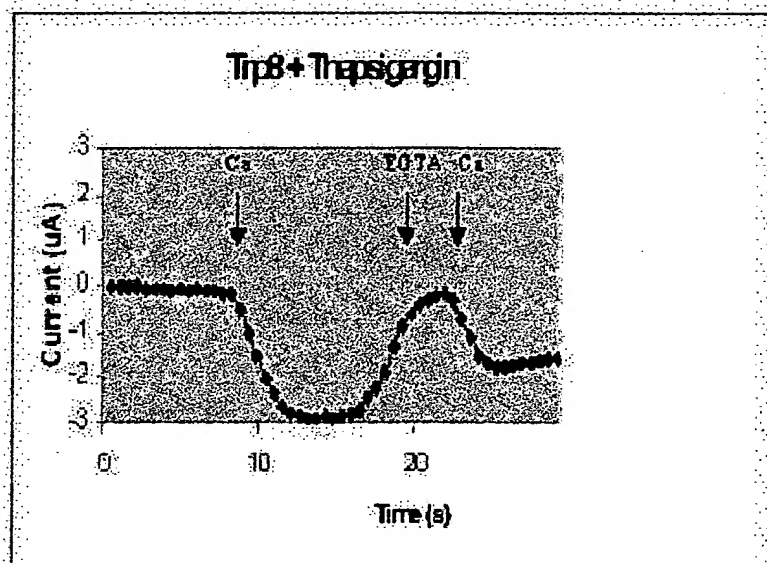


Figure 12  
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Injected with:                      H2O                      TRP8 cRNA

Thapsigargin 2uM:    +                      -                      +                      -

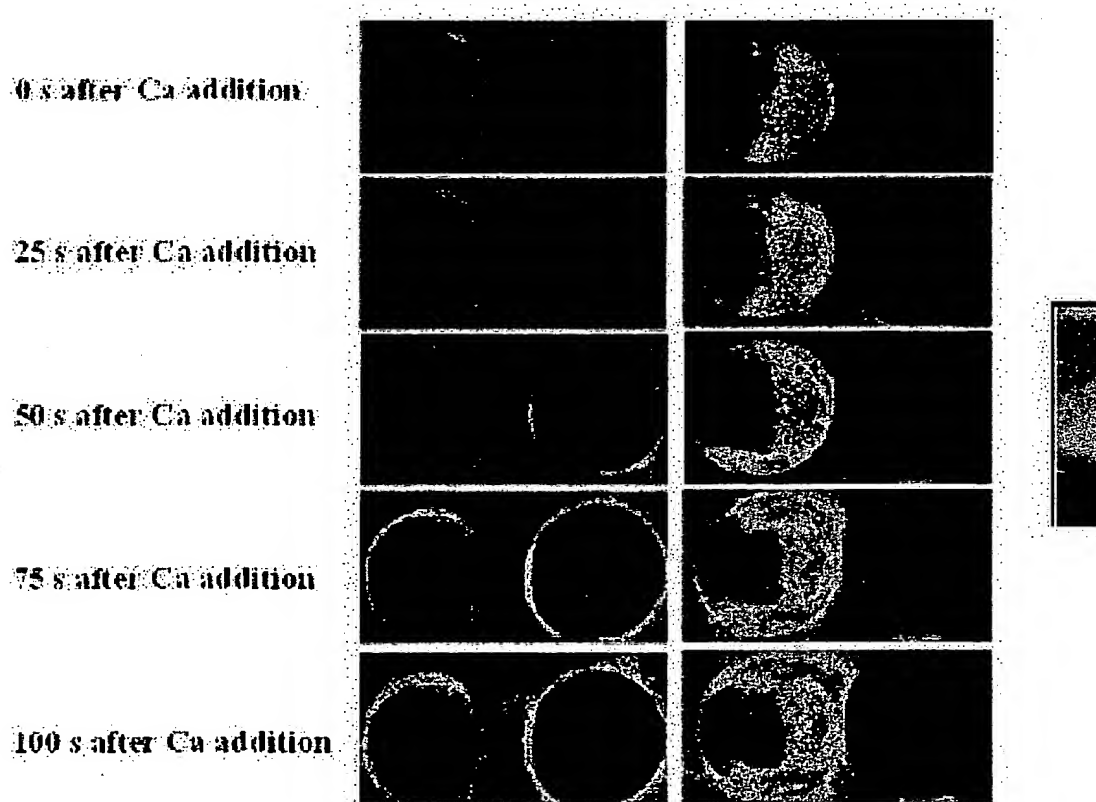
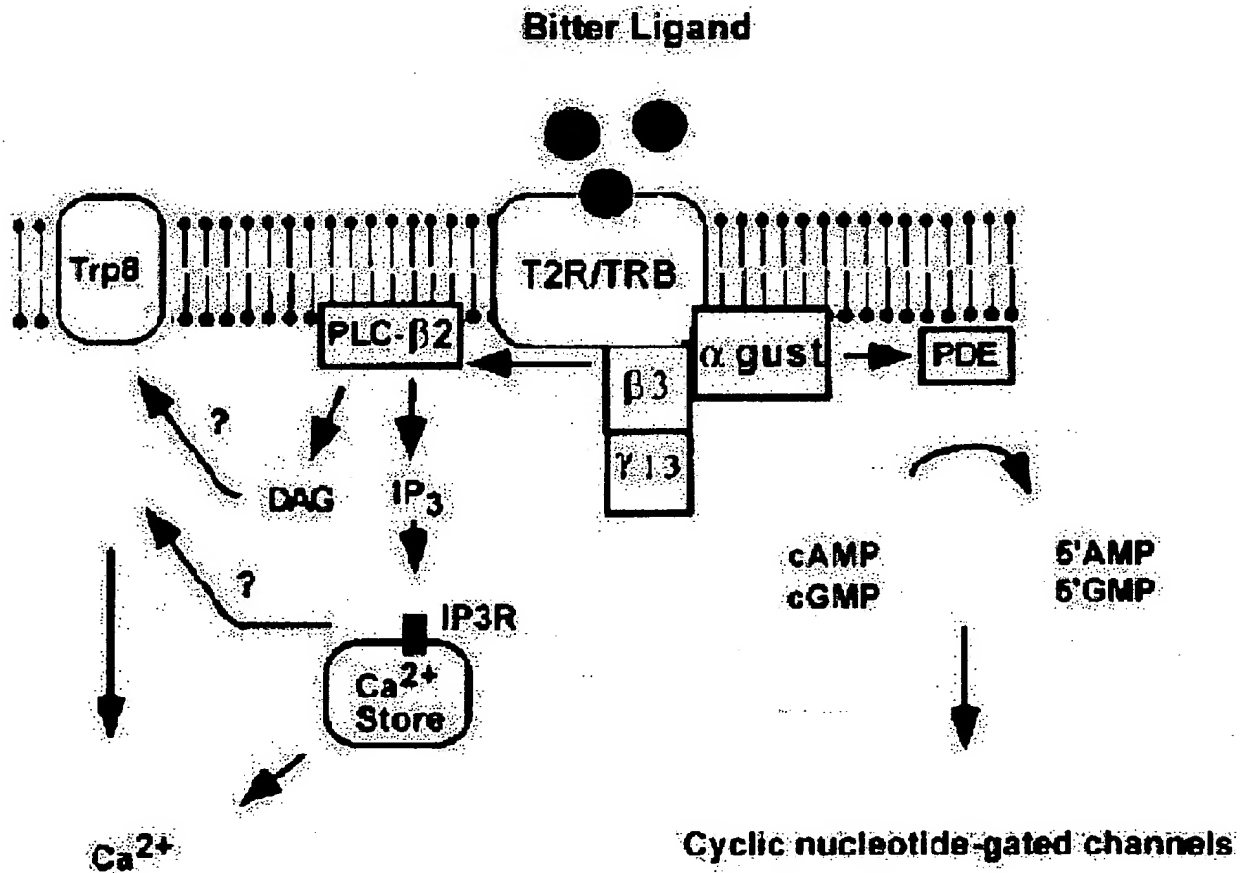


Figure 13  
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## Transduction of Taste Stimuli



Modified from Kinnamon, Neuron (2000) 25:507-510

Figure 14  
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